



04-18-23

Box 5-29-

1646

Attorney Docket No. 5470-130DV

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re: French et al.  
Serial No.: 09/497,822  
Filed: February 3, 2000

Confirmation No. 7943  
Group Art Unit: 1646  
Examiner: M. Pak

For: ANDROGEN RECEPTOR PROTEINS, RECOMBINANT DNA MOLECULES  
CODING FOR SUCH, AND USE OF SUCH COMPOSITIONS

Date: April 16, 2003

BOX SEQUENCE  
PO Box 2327  
Arlington, VA 22202

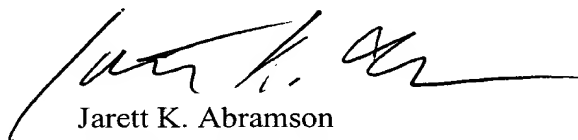
22/E  
D. J. J  
4/23/03  
**RECEIVED**  
APR 21 2003  
TECH CENTER 1600/2900

**STATEMENT IN SUPPORT OF FILING A  
SEQUENCE LISTING UNDER 37 CFR § 1.821(f)**

Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence listing are the same. I also hereby state as required by 37 CFR § 1.821(h) that the computer readable copy submitted concurrently herewith contains no new matter, nor does it go beyond the disclosure of the application as filed.

Respectfully submitted,

  
Jarett K. Abramson  
Registration No. 47,376



20792

PATENT TRADEMARK OFFICE

**CERTIFICATE OF EXPRESS MAILING**

Express Mail Label No. EV 193631883 US

Date of Deposit: April 16, 2003

I hereby certify that this correspondence is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 on the date indicated above and is addressed to: BOX SEQUENCE, PO Box 2327, Arlington, VA 22202

  
Clara R. Beard



SEQUENCE LISTING

<110> French, Frank  
Wilson, Elizabeth  
Joseph, David  
Lubahn, Dennis

<120> ANDROGEN RECEPTOR PROTEINS RECOMBINANT DNA MOLECULES AND CODING  
FOR SUCH AND USE OF SUCH COMPOSITIONS

<130> 5470-130DV

<140> US 09/497,822

<141> 2000-02-03

<160> 26

<170> PatentIn version 3.1

<210> 1

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 1

acctgtgagg gctgtaaggt cttcttcaaa ag

32

<210> 2

<211> 32

<212> DNA

<213> Homo sapiens

<400> 2

acatgtggaa gctgcaaggt cttcttcaaa ag

32

<210> 3

<211> 32

<212> DNA

<213> Homo sapiens

<400> 3

acctgtggga gctgtaaggt cttctttaag ag

32

<210> 4

<211> 32

<212> DNA

<213> Homo sapiens

<400> 4

acctgtggca gctgcaaagt tttcttcaaa ag

32

<210> 5

<211> 32

<212> DNA

RECEIVED  
APR 21 2003  
TECH CENTER 1600/2900

<213> Homo sapiens

<400> 5

acttgtaggaa gctgtaaagt tttcttcaaa ag

32

<210> 6

<211> 32

<212> DNA

<213> Homo sapiens

<400> 6

tcctgtgagg gctgtaaggc cttcttcaag ag

32

<210> 7

<211> 32

<212> DNA

<213> Homo sapiens

<400> 7

acgtgtgaag gctgcaaggg tttctttaga ag

32

<210> 8

<211> 32

<212> DNA

<213> Homo sapiens

<400> 8

gcctgtgagg gctgcaaggg cttcttccgc cg

32

<210> 9

<211> 66

<212> PRT

<213> Homo sapiens

<400> 9

Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu  
1 5 10 15

Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys  
20 25 30

Gln Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe  
35 40 45

Arg Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala  
50 55 60

Gly Met  
65

<210> 10

El  
Cont

<211> 66  
 <212> PRT  
 <213> Homo sapiens

<400> 10

Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Val Leu  
 1 5 10 15

Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Met Glu Gly Gln  
 20 25 30

His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile Val Asp Lys Ile  
 35 40 45

Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu Arg Lys Cys Cys Gln Ala  
 50 55 60

Gly Met  
 65

<210> 11  
 <211> 66  
 <212> PRT  
 <213> Homo sapiens

<400> 11

Cys Leu Val Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Val Val  
 1 5 10 15

Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Val Glu Gly Gln  
 20 25 30

His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile Ile Asp Lys Ile  
 35 40 45

Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu Gln Lys Cys Leu Gln Ala  
 50 55 60

Gly Met  
 65

<210> 12  
 <211> 66  
 <212> PRT  
 <213> Homo sapiens

<400> 12

Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His Tyr Gly Val Leu



Ala Met Phe Thr Cys Pro Phe Asn Gly Asp Cys Lys Ile Thr Lys Asp  
 35 40 45

Asn Arg Arg His Cys Gln Ala Cys Arg Leu Lys Arg Cys Val Asp Ile  
 50 55 60

Gly Met  
 65

<210> 15  
 <211> 68  
 <212> PRT  
 <213> Homo sapiens

<400> 15

Cys Val Val Cys Gly Asp Lys Ala Thr Gly Tyr His Tyr Arg Cys Ile  
 1 5 10 15

Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile Gln Lys Asn  
 20 25 30

Leu His Pro Ser Tyr Ser Cys Lys Tyr Glu Gly Lys Cys Val Ile Asp  
 35 40 45

Lys Val Thr Arg Asn Gln Cys Gln Glu Cys Arg Phe Lys Lys Cys Ile  
 50 55 60

Tyr Val Gly Met  
 65

<210> 16  
 <211> 68  
 <212> PRT  
 <213> Avian erythroblastosis virus

<400> 16

Cys Val Val Cys Gly Asp Lys Ala Thr Gly Tyr His Tyr Arg Cys Ile  
 1 5 10 15

Thr Cys Glu Gly Cys Lys Ser Phe Phe Arg Arg Thr Ile Gln Lys Asn  
 20 25 30

Leu His Pro Thr Thr Ser Cys Thr Tyr Asp Gly Cys Cys Val Ile Asp  
 35 40 45

Lys Ile Thr Arg Asn Gln Cys Gln Leu Cys Arg Phe Lys Lys Cys Ile  
 50 55 60

Ser Val Gly Met  
65

<210> 17  
<211> 66  
<212> PRT  
<213> Homo sapiens

<400> 17

Cys Phe Val Cys Gln Asp Lys Ser Ser Gly Tyr His Tyr Gly Val Ser  
1 5 10 15

Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Gln Lys Asn  
20 25 30

Met Val Tyr Thr Cys His Arg Asp Lys Asn Cys Ile Ile Asn Lys Val  
35 40 45

Thr Arg Asn Arg Cys Gln Tyr Cys Arg Leu Gln Lys Cys Phe Glu Val  
50 55 60

Gly Met  
65

<210> 18  
<211> 5082  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (360)..(360)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (365)..(365)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (376)..(376)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (385)..(385)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (399)..(399)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (407)..(407)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (417)..(417)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (422)..(422)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (435)..(435)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (439)..(439)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (441)..(441)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (598)..(598)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (689)..(689)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (714)..(715)  
<223> "n" denotes any nucleotide

<220>



<221> misc\_feature  
<222> (844)..(844)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (870)..(870)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (918)..(918)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (932)..(932)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (1195)..(1195)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (1198)..(1198)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (1202)..(1202)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (1248)..(1248)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (1322)..(1322)  
<223> "n" denotes any nucleotide

<220>  
<221> CDS  
<222> (1864)..(4632)  
<223>

<400> 18  
gagctctgga caaaattgag cgcctatgtg tacatggcaa gtgttttttag tgtttgtgtg

60

tttacctgct tgtctgggtg attttgcctt tgagagtctg gatgagaaat gcatgggttaa	120
aggcaattcc agacaggaag aaaggcagag aagagggtag aaatgacctc tgattcttgg	180
ggctgaggggt tcctagagca aatggcacaa tgccacgagg cccgatctat ccctatgacg	240
gaactctaag gtttcagcat cagctatctg ctggccttgg cactggcctg cctcctcagt	300
ttgtaggaga ctctcccact ctcccactctg cgcgctctta tcagtcctga aaagaaccn	360
tggcnagcca ggagcnaggt attcntatcg tccttttctt cctcctngcc tcacctngtt	420
gntttttaga ttggncttng naaccaaatt tgtatgctgg cctccaggaa atctggagcc	480
tggcgccctaa accttggttt aggaaagcag gagctattca ggaagcaggg tcctccaggg	540
ctagagctag cctctcctgc cctcgccac gtgcgccagc acttgtttct ccaaagcnac	600
taggcaggcg ttagcgcgcg gtgaggggag gggagaaaag gaaaggggag gggagggaaa	660
aggaggtggg aaggcaagga ggccggccng gtgggggcgg gaccgcactc gcannaactg	720
ttgcatttgc tctccacctc ccagcgcccc ctccgagatc ccggggagcc agcttgctgg	780
gagagcggga acgggtccgga gcaagcccag aggcagagga ggcgacagag ggaaaaaggg	840
cccnagctag ccgctccagt gctgtacagn agccgaagga cgcaccacgc cagccccagc	900
ccggctccag cgacagcnaa cgctcttgc ancggttcga agccgcgcgc cggagctgcc	960
ctttcctctt cgggtgaagt tttaaaagct gctaaagact cggaggaagc aaggaaagtg	1020
cctggtagga ctgacggctg cctttgtcct cctcctctcc accccgcctc cccccacct	1080
gccttcccc cctccccgt cttctctccc gcagctgcct cagtcggcta ctctcagcca	1140
acccccctca ccaccttct cccccccgc cccccgcgc ccgtcggccc agcgnatgnca	1200
gnccgagttt gcagagaggt aactccctt ggctgcgagc gggcgagnct agctgcacat	1260
tgcaaagaag gctcttagga gcaggcgact ggggagcggc ttcagcactg cagccacgac	1320
cngcctgggt aggctgcacg cggagagaac cctctgtttt cccccactct ctctccacct	1380
cctcctgcct tccccacccc gagtgcgag ccagagatca aaagatgaaa aggcagtcag	1440
gtcttcagta gccaaaaaac aaaacaaaca aaaacaaaa agccgaaata aaagaaaaag	1500
ataataactc agttcttatt tgcacctact tcagtggaca ctgaatttgg aaggtaggag	1560
attttgttt tttcttttaa gatctgggca tcttttgaat ctacccttca agtattaaga	1620
gacagactgt gagcctagca gggcagatct tgtccaccgt gtgtcttctt ctgcacgaga	1680
ctttgaggct gtcagagcgc tttttgcgtg gttgctccc caagtttct tctctggagc	1740
ttcccgcagg tgggcagcta gctgcagcga ctaccgcac atcacagcct gttgaactct	1800
tctgagcaag agaaggggag gcggggtaag ggaagtaggt ggaagattca gccaaagctca	1860

agg atg gaa gtg cag tta ggg ctg gga agg gtc tac cct cgg ccg ccg	1908
Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro	
1 5 10 15	
tcc aag acc tac cga gga gct ttc cag aat ctg ttc cag agc gtg cgc	1956
Ser Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg	
20 25 30	
gaa gtg atc cag aac ccg ggc ccc agg cac cca gag gcc gcg agc gca	2004
Glu Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala	
35 40 45	
gca cct ccc ggc gcc agt ttg ctg ctg ctg cag cag cag cag cag cag	2052
Ala Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln	
50 55 60	
cag cag cag cag cag cag cag cag cag cag cag cag cag cag cag	2100
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln	
65 70 75	
cag cag caa gag act agc ccc agg cag cag cag cag cag cag ggt gag	2148
Gln Gln Gln Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu	
80 85 90 95	
gat ggt tct ccc caa gcc cat cgt aga ggc ccc aca ggc tac ctg gtc	2196
Asp Gly Ser Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val	
100 105 110	
ctg gat gag gaa cag caa cct tca cag ccg cag tcg gcc ctg gag tgc	2244
Leu Asp Glu Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys	
115 120 125	
cac ccc gag aga ggt tgc gtc cca gag cct gga gcc gcc gtg gcc gcc	2292
His Pro Glu Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala	
130 135 140	
agc aag ggg ctg ccg cag cag ctg cca gca cct ccg gac gag gat gac	2340
Ser Lys Gly Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp	
145 150 155	
tca gct gcc cca tcc acg ttg tcc ctg ctg ggc ccc act ttc ccc ggc	2388
Ser Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly	
160 165 170 175	
tta agc agc tgc tcc gct gac ctt aaa gac atc ctg agc gag gcc agc	2436
Leu Ser Ser Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser	
180 185 190	
acc atg caa ctc ctt cag caa cag cag cag gaa gca gta tcc gaa ggc	2484
Thr Met Gln Leu Leu Gln Gln Gln Gln Glu Ala Val Ser Glu Gly	
195 200 205	
agc agc agc ggg aga gcg agg gag gcc tcg ggg gct ccc act tcc tcc	2532
Ser Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser	
210 215 220	
aag gac aat tac tta ggg ggc act tcg acc att tct gac aac gcc aag	2580
Lys Asp Asn Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys	
225 230 235	
gag ttg tgt aag gca gtg tcg gtg tcc atg ggc ctg ggt gtg gag gcg	2628

Glu	Leu	Cys	Lys	Ala	Val	Ser	Val	Ser	Met	Gly	Leu	Gly	Val	Glu	Ala	
240					245					250					255	
ttg	gag	cat	ctg	agt	cca	ggg	gaa	cag	ctt	cgg	ggg	gat	tgc	atg	tac	2676
Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu	Arg	Gly	Asp	Cys	Met	Tyr	
				260					265					270		
gcc	cca	ctt	ttg	gga	gtt	cca	ccc	gct	gtg	cgt	ccc	act	cct	tgt	gcc	2724
Ala	Pro	Leu	Leu	Gly	Val	Pro	Pro	Ala	Val	Arg	Pro	Thr	Pro	Cys	Ala	
			275					280					285			
cca	ttg	gcc	gaa	tgc	aaa	ggt	tct	ctg	cta	gac	gac	agc	gca	ggc	aag	2772
Pro	Leu	Ala	Glu	Cys	Lys	Gly	Ser	Leu	Leu	Asp	Asp	Ser	Ala	Gly	Lys	
		290					295					300				
agc	act	gaa	gat	act	gct	gag	tat	tcc	cct	ttc	aag	gga	ggg	tac	acc	2820
Ser	Thr	Glu	Asp	Thr	Ala	Glu	Tyr	Ser	Pro	Phe	Lys	Gly	Gly	Tyr	Thr	
	305					310					315					
aaa	ggg	cta	gaa	ggc	gag	agc	cta	ggc	tgc	tct	ggc	agc	gct	gca	gca	2868
Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys	Ser	Gly	Ser	Ala	Ala	Ala	
320					325				330						335	
ggg	agc	tcc	ggg	aca	ctt	gaa	ctg	ccg	tct	acc	ctg	tct	ctc	tac	aag	2916
Gly	Ser	Ser	Gly	Thr	Leu	Glu	Leu	Pro	Ser	Thr	Leu	Ser	Leu	Tyr	Lys	
				340				345						350		
tcc	gga	gca	ctg	gac	gag	gca	gct	gcg	tac	cag	agt	cgc	gac	tac	tac	2964
Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr	Gln	Ser	Arg	Asp	Tyr	Tyr	
			355					360					365			
aac	ttt	cca	ctg	gct	ctg	gcc	gga	ccg	ccg	ccc	cct	ccg	ccg	cct	ccc	3012
Asn	Phe	Pro	Leu	Ala	Leu	Ala	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	
		370					375					380				
cat	ccc	cac	gct	cgc	atc	aag	ctg	gag	aac	ccg	ctg	gac	tac	ggc	agc	3060
His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn	Pro	Leu	Asp	Tyr	Gly	Ser	
	385					390					395					
gcc	tgg	gcg	gct	gcg	gcg	gcg	cag	tgc	cgc	tat	ggg	gac	ctg	gcg	agc	3108
Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Ala	Ser	
400					405				410						415	
ctg	cat	ggc	gcg	ggt	gca	gcg	gga	ccc	ggt	tct	ggg	tca	ccc	tca	gcc	3156
Leu	His	Gly	Ala	Gly	Ala	Ala	Gly	Pro	Gly	Ser	Gly	Ser	Pro	Ser	Ala	
				420				425						430		
gcc	gct	tcc	tca	tcc	tgg	cac	act	ctc	ttc	aca	gcc	gaa	gaa	ggc	cag	3204
Ala	Ala	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	
			435					440					445			
ttg	tat	gga	ccg	tgt	ggt	ggt	ggt	ggg	ggt	ggt	ggc	ggc	ggc	ggc	ggc	3252
Leu	Tyr	Gly	Pro	Cys	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
		450					455					460				
ggc	ggc	ggc	ggc	ggc	ggc	ggc	ggc	ggc	ggc	ggc	ggc	ggc	gag	gcg	gga	3300
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Glu	Ala	Gly	
		465					470					475				
gct	gta	gcc	ccc	tac	ggc	tac	act	cgg	ccc	cct	cag	ggg	ctg	gcg	ggc	3348
Ala	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Gly	

480	485	490	495	
cag gaa agc gac ttc acc gca cct gat gtg tgg tac cct ggc ggc atg Gln Glu Ser Asp Phe Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met 500 505 510				3396
gtg agc aga gtg ccc tat ccc agt ccc act tgt gtc aaa agc gaa atg Val Ser Arg Val Pro Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met 515 520 525				3444
ggc ccc tgg atg gat agc tac tcc gga cct tac ggg gac atg cgt ttg Gly Pro Trp Met Asp Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu 530 535 540				3492
gag act gcc agg gac cat gtt ttg ccc att gac tat tac ttt cca ccc Glu Thr Ala Arg Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro 545 550 555				3540
cag aag acc tgc ctg atc tgt gga gat gaa gct tct ggg tgt cac tat Gln Lys Thr Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr 560 565 570 575				3588
gga gct ctc aca tgt gga agc tgc aag gtc ttc ttc aaa aga gcc gct Gly Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala 580 585 590				3636
gaa ggg aaa cag aag tac ctg tgc gcc agc aga aat gat tgc act att Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile 595 600 605				3684
gat aaa ttc cga agg aaa aat tgt cca tct tgt cgt ctt cgg aaa tgt Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys 610 615 620				3732
tat gaa gca ggg atg act ctg gga gcc cgg aag ctg aag aaa ctt ggt Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly 625 630 635				3780
aat ctg aaa cta cag gag gaa gga gag gct tcc agc acc acc agc ccc Asn Leu Lys Leu Gln Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro 640 645 650 655				3828
act gag gag aca acc cag aag ctg aca gtg tca cac att gaa ggc tat Thr Glu Glu Thr Thr Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr 660 665 670				3876
gaa tgt cag ccc atc ttt ctg aat gtc ctg gaa gcc att gag cca ggt Glu Cys Gln Pro Ile Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly 675 680 685				3924
gta gtg tgt gct gga cac gac aac aac cag ccc gac tcc ttt gca gcc Val Val Cys Ala Gly His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala 690 695 700				3972
ttg ctc tct agc ctc aat gaa ctg gga gag aga cag ctt gta cac gtg Leu Leu Ser Ser Leu Asn Gln Leu Gly Glu Arg Gln Leu Val His Val 705 710 715				4020
gtc aag tgg gcc aag gcc ttg cct ggc ttc cgc aac tta cac gtg gac Val Lys Trp Ala Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp 720 725 730 735				4068

gac cag atg gct gtc att cag tac tcc tgg atg ggg ctc atg gtg ttt Asp Gln Met Ala Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe 740 745 750	4116
gcc atg ggc tgg cga tcc ttc acc aat gtc aac tcc agg atg ctc tac Ala Met Gly Trp Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr 755 760 765	4164
ttc gcc cct gat ctg gtt ttc aat gag tac cgc atg cac aag tcc cgg Phe Ala Pro Asp Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg 770 775 780	4212
atg tac agc cag tgt gtc cga atg agg cac ctc tct caa gag ttt gga Met Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly 785 790 795	4260
tgg ctc caa atc acc ccc cag gaa ttc ctg tgc atg aaa gca ctg cta Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu 800 805 810 815	4308
ctc ttc agc att att cca gtg gat ggg ctg aaa aat caa aaa ttc ttt Leu Phe Ser Ile Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe 820 825 830	4356
gat gaa ctt cga atg aac tac atc aag gaa ctc gat cgt atc att gca Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala 835 840 845	4404
tgc aaa aga aaa aat ccc aca tcc tgc tca aga cgc ttc tac cag ctc Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu 850 855 860	4452
acc aag ctc ctg gac tcc gtg cag cct att gcg aga gag ctg cat cag Thr Lys Leu Leu Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln 865 870 875	4500
ttc act ttt gac ctg cta atc aag tca cac atg gtg agc gtg gac ttt Phe Thr Phe Asp Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe 880 885 890 895	4548
ccg gaa atg atg gca gag atc atc tct gtg caa gtg ccc aag atc ctt Pro Glu Met Met Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu 900 905 910	4596
tct ggg aaa gtc aag ccc atc tat ttc cac acc cag tgaagcattg Ser Gly Lys Val Lys Pro Ile Tyr Phe His Thr Gln 915 920	4642
gaaaccctat tccccacccc cagctcatgc cccctttcag atgtcttctg cctgtttataa	4702
ctctgcacta ctctcttgca gtgccttggg gaatttcctc tattgatgta cagtctgtca	4762
tgaacatggt cctgaattct atttgctggg cttttttttt ctctttctct cctttctttt	4822
tcttttcccc tccctatcta accctcccat ggcaccttca gactttgctt cccattgtgg	4882
ctcctatctg tgttttgaat ggtgttgat gcctttaaat ctgtgatgat cctcatatgg	4942
cccagtgtea agttgtgctt gtttacagca ctactctgtg ccagccacac aaacgtttac	5002

ttatcttatg ccacgggaag tttagagagc taagattatc tggggaaatc aaaacaaaaa 5062  
acaagcaaac aaaaaaaaaa 5082

<210> 19  
<211> 923  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (360)..(360)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (365)..(365)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (376)..(376)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (385)..(385)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (399)..(399)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (407)..(407)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (417)..(417)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (422)..(422)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (435)..(435)  
<223> "n" denotes any nucleotide

<220>  
<221> misc\_feature  
<222> (439)..(439)  
<223> "n" denotes any nucleotide

<220>

```

<221> misc_feature
<222> (441)..(441)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (598)..(598)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (689)..(689)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (714)..(715)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (844)..(844)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (870)..(870)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (918)..(918)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (932)..(932)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (1195)..(1195)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (1198)..(1198)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (1202)..(1202)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (1248)..(1248)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature

```



<222> (1322)..(1322)

<223> "n" denotes any nucleotide

<400> 19

Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser  
1 5 10 15

Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu  
20 25 30

Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala  
35 40 45

Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln  
50 55 60

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln  
65 70 75 80

Gln Gln Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp  
85 90 95

Gly Ser Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu  
100 105 110

Asp Glu Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His  
115 120 125

Pro Glu Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser  
130 135 140

Lys Gly Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser  
145 150 155 160

Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu  
165 170 175

Ser Ser Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr  
180 185 190

Met Gln Leu Leu Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser  
195 200 205

Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys  
210 215 220

Asp Asn Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu  
 225 230 235 240

Leu Cys Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu  
 245 250 255

Glu His Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala  
 260 265 270

Pro Leu Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro  
 275 280 285

Leu Ala Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser  
 290 295 300

Thr Glu Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys  
 305 310 315 320

Gly Leu Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly  
 325 330 335

Ser Ser Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser  
 340 345 350

Gly Ala Leu Asp Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn  
 355 360 365

Phe Pro Leu Ala Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro His  
 370 375 380

Pro His Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala  
 385 390 395 400

Trp Ala Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu  
 405 410 415

His Gly Ala Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala  
 420 425 430

Ala Ser Ser Ser Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu  
 435 440 445

Tyr Gly Pro Cys Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 450 455 460

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly Ala

465		470		475		480									
Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Gly	Gln
				485					490					495	
Glu	Ser	Asp	Phe	Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	Gly	Met	Val
			500					505					510		
Ser	Arg	Val	Pro	Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	Glu	Met	Gly
		515					520					525			
Pro	Trp	Met	Asp	Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu	Glu
	530					535					540				
Thr	Ala	Arg	Asp	His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln
545					550					555					560
Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly
			565						570					575	
Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu
			580					585					590		
Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp
		595					600					605			
Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr
	610					615					620				
Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn
625					630					635					640
Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	Ser	Pro	Thr
				645					650					655	
Glu	Glu	Thr	Thr	Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr	Glu
			660					665					670		
Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val
		675					680					685			
Val	Cys	Ala	Gly	His	Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu
	690					695					700				
Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly	Glu	Arg	Gln	Leu	Val	His	Val	Val
705				710						715					720

Lys Trp Ala Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp  
725 730 735

Gln Met Ala Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala  
740 745 750

Met Gly Trp Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe  
755 760 765

Ala Pro Asp Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met  
770 775 780

Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp  
785 790 795 800

Leu Gln Ile Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu  
805 810 815

Phe Ser Ile Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp  
820 825 830

Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys  
835 840 845

Lys Arg Lys Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr  
850 855 860

Lys Leu Leu Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe  
865 870 875 880

Thr Phe Asp Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro  
885 890 895

Glu Met Met Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser  
900 905 910

Gly Lys Val Lys Pro Ile Tyr Phe His Thr Gln  
915 920

<210> 20

<211> 4289

<212> DNA

<213> Rattus rattus

<220>

<221> CDS

<222> (1123) .. (3828)  
 <223>

<400> 20  
 aattcgggaa ggatcgagca aaccaggaaa gtaaggatgg agatcctagg agagtgtcca 60  
 tgccctgaaa ggagcccacc aaagatgaac tgttgcatTTt gctttccacc tcccagcgcc 120  
 ccctcggaga tccctaggag ccagcctgct gggagaacca gaggggtccgg agcaaacctg 180  
 gaggctgaga gggcatcaga ggggaaaaga ctgagttagc cactccagtg ccatacagaa 240  
 gcttaagggga cataccacgc cagccccagc ccagcgacag ccaacgcctg ttgcagagcg 300  
 gcggttcga agccgcccgc cagaagctgc cttttcctct tcggtgaagt ttctaaaagc 360  
 tgcgggagac tcggaggaag cgaagaaagt gtccggtagg actacgactg cttttgtcct 420  
 cctccctcct acccctaccc ctcttggtgc cctctccct gagcggacta ggcaggcttc 480  
 ctggccagcc ctctccccta caccaccagc tctgccagcc agtttgcaca gaggtaactc 540  
 cttttggctg aaagcagacg agcttggtgc ccattggaag ggaggctttt gggagcccag 600  
 agactgagga gcaacagcac gctggagagt ccttgattcc aggttctccc ccctgcacct 660  
 cctactgccc gcccctcacc ctgtgtgtgc agctagaatt gaaaagatga aaagacagtt 720  
 ggggcttcag tagtcgaaag caaaacaaaa gcaaaaagaa aacaaaaaga aaatagccca 780  
 gttcttattt gcacctgctt cagtggacat tgactttgga aggcagagaa ttttccttcc 840  
 cccagtgcaa gctttgagca tcttttaatc tgttcttcaa gtatttaggg acaaactgtg 900  
 aaactagcag ggcagatcct gtctagcgcg tgccttcctt tacaggagac tttgaggcta 960  
 tctgggcgct cccccccctc cctgcaagtt ttcttcctg gagcttcccg caggtgggca 1020  
 gctagctgca gatactacat catcagtcag tagaactctt cagagcaaga gacgaggagg 1080  
 caggataagg gaattcgggtg gaagctagag acaagctaaa gg atg gag gtg cag 1134  
 Met Glu Val Gln  
 1  
 tta ggg ctg gga agg gtc tac cca cgg ccc ccg tcc aag acc tat cga 1182  
 Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser Lys Thr Tyr Arg  
 5 10 15 20  
 gga gcg ttc cag aat ctg ttc cag agc gtg cgc gaa gcg atc cag aac 1230  
 Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu Ala Ile Gln Asn  
 25 30 35  
 ccg ggc ccc agg cac cct gag gcc gct agc ata gca cct ccc ggt gcc 1278  
 Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ile Ala Pro Pro Gly Ala  
 40 45 50  
 tgt tta cag cag cgg cag gag act agc ccc cgg cgg cgg cgg cgg cag 1326  
 Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg Arg Arg Arg Gln  
 55 60 65

cag	cac	cct	gag	gat	ggc	tct	cct	caa	gcc	cac	atc	aga	ggc	acc	aca	1374
Gln	His	Pro	Glu	Asp	Gly	Ser	Pro	Gln	Ala	His	Ile	Arg	Gly	Thr	Thr	
70						75					80					
ggc	tac	ctg	ggc	ctg	gag	gag	gaa	cag	cag	cct	tca	cag	cag	cag	tca	1422
Gly	Tyr	Leu	Ala	Leu	Glu	Glu	Glu	Gln	Gln	Pro	Ser	Gln	Gln	Gln	Ser	
85					90					95					100	
gcc	tcc	gag	ggc	cac	cct	gag	agc	ggc	tgc	ctc	ccg	gag	cct	gga	gct	1470
Ala	Ser	Glu	Gly	His	Pro	Glu	Ser	Gly	Cys	Leu	Pro	Glu	Pro	Gly	Ala	
				105					110					115		
gcc	acg	gct	cct	ggc	aag	ggg	ctg	ccg	cag	cag	cca	cca	gct	cct	cca	1518
Ala	Thr	Ala	Pro	Gly	Lys	Gly	Leu	Pro	Gln	Gln	Pro	Pro	Ala	Pro	Pro	
			120					125					130			
gat	cag	gat	gac	tca	gct	gcc	cca	tcc	acg	ttg	tcc	cta	ctg	ggc	ccc	1566
Asp	Gln	Asp	Asp	Ser	Ala	Ala	Pro	Ser	Thr	Leu	Ser	Leu	Leu	Gly	Pro	
			135				140					145				
act	ttc	cca	ggc	tta	agc	agc	tgc	tcc	gca	gac	att	aaa	gac	atc	ctg	1614
Thr	Phe	Pro	Gly	Leu	Ser	Ser	Cys	Ser	Ala	Asp	Ile	Lys	Asp	Ile	Leu	
	150					155					160					
agc	gag	ggc	ggc	acc	atg	caa	ctt	ctt	cag	cag	cag	cag	caa	cag	caa	1662
Ser	Glu	Ala	Gly	Thr	Met	Gln	Leu	Leu	Gln	Gln	Gln	Gln	Gln	Gln	Gln	
165					170				175						180	
cag	cag	cag	cag	cag	cag	cag	cag	cag	cag	cag	caa	cag	cag	cag	gag	1710
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Glu	
				185				190							195	
gta	ata	tcc	gaa	ggc	agc	agc	agc	gtg	aga	gca	agg	gag	gcc	act	ggg	1758
Val	Ile	Ser	Glu	Gly	Ser	Ser	Ser	Val	Arg	Ala	Arg	Glu	Ala	Thr	Gly	
			200					205					210			
gct	ccc	tct	tcc	tcc	aag	gat	agt	tac	cta	ggg	ggc	aat	tcg	acc	ata	1806
Ala	Pro	Ser	Ser	Ser	Lys	Asp	Ser	Tyr	Leu	Gly	Gly	Asn	Ser	Thr	Ile	
		215				220						225				
tct	gac	agt	ggc	aag	gag	ttg	tgt	aaa	gca	gtg	tct	gtg	tcc	atg	ggg	1854
Ser	Asp	Ser	Ala	Lys	Glu	Leu	Cys	Lys	Ala	Val	Ser	Val	Ser	Met	Gly	
	230					235					240					
ttg	ggt	gtg	gaa	gca	ctg	gaa	cat	ctg	agt	cca	ggg	gag	cag	ctt	cgg	1902
Leu	Gly	Val	Glu	Ala	Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu	Arg	
245					250					255					260	
ggc	gac	tgc	atg	tac	gcg	tcg	ctc	ctg	gga	ggg	cca	ccc	ggc	gtg	cgt	1950
Gly	Asp	Cys	Met	Tyr	Ala	Ser	Leu	Leu	Gly	Gly	Pro	Pro	Ala	Val	Arg	
				265					270					275		
ccc	act	cct	tgt	gcg	cct	ctg	gcc	gaa	tgc	aaa	ggg	ctt	tcc	ctg	gac	1998
Pro	Thr	Pro	Cys	Ala	Pro	Leu	Ala	Glu	Cys	Lys	Gly	Leu	Ser	Leu	Asp	
			280					285					290			
gaa	ggc	ccg	ggc	aaa	ggc	act	gaa	gag	act	gct	gag	tat	tcc	tct	ttc	2046
Glu	Gly	Pro	Gly	Lys	Gly	Thr	Glu	Glu	Thr	Ala	Glu	Tyr	Ser	Ser	Phe	
		295					300					305				
aag	gga	ggt	tac	gcc	aaa	ggg	ttg	gaa	ggg	gag	agt	ctg	ggc	tgc	tct	2094

Lys	Gly	Gly	Tyr	Ala	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys	Ser		
310						315					320						
ggc	agc	agt	gaa	gca	ggc	agc	tct	ggg	aca	ctt	gag	atc	ccg	tcc	tca	2142	
Gly	Ser	Ser	Glu	Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Ile	Pro	Ser	Ser		
325					330					335					340		
ctg	tct	ctg	tat	aag	tct	gga	gca	gta	gac	gag	gca	gca	gca	tac	cag	2190	
Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Val	Asp	Glu	Ala	Ala	Ala	Tyr	Gln		
				345					350					355			
aat	cgc	gac	tac	tac	aac	ttt	ccg	ctc	gct	ctg	tcc	ggg	ccg	ccg	cac	2238	
Asn	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ser	Gly	Pro	Pro	His		
			360					365					370				
ccc	ccg	ccc	cct	acc	cat	cca	cac	gcc	cgc	atc	aag	ctg	gag	aac	ccg	2286	
Pro	Pro	Pro	Pro	Thr	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn	Pro		
		375					380					385					
tcg	gac	tac	ggc	agc	gcc	tgg	gct	gcg	gcg	gca	gcg	caa	tgc	cgc	tat	2334	
Ser	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg	Tyr		
	390					395					400						
ggg	gac	ttg	gct	agc	cta	cat	gga	ggg	agt	gta	gcc	gga	ccc	agc	act	2382	
Gly	Asp	Leu	Ala	Ser	Leu	His	Gly	Gly	Ser	Val	Ala	Gly	Pro	Ser	Thr		
405					410					415					420		
gga	tcg	ccc	cca	gcc	acc	gcc	tct	tct	tcc	tgg	cat	act	ctc	ttc	aca	2430	
Gly	Ser	Pro	Pro	Ala	Thr	Ala	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe	Thr		
				425					430					435			
gct	gaa	gaa	ggc	caa	tta	tat	ggg	cca	gga	ggc	ggg	ggc	ggc	agc	agt	2478	
Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Ser	Ser		
			440					445					450				
agc	cca	agc	gat	gct	ggg	cct	gta	gcc	ccc	tat	ggc	tac	act	cgg	ccc	2526	
Ser	Pro	Ser	Asp	Ala	Gly	Pro	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	Pro		
		455				460					465						
cct	cag	ggg	ctg	gca	agc	cag	gag	ggc	gac	ttc	tct	gcc	tct	gaa	gtg	2574	
Pro	Gln	Gly	Leu	Ala	Ser	Gln	Glu	Gly	Asp	Phe	Ser	Ala	Ser	Glu	Val		
	470					475					480						
tgg	tat	cct	ggc	gga	gtt	gtg	aac	aga	gtc	ccc	tat	ccc	agt	ccc	agt	2622	
Trp	Tyr	Pro	Gly	Gly	Val	Val	Asn	Arg	Val	Pro	Tyr	Pro	Ser	Pro	Ser		
485					490					495					500		
tgt	gtt	aaa	agt	gaa	atg	gga	cct	tgg	atg	gag	aac	tac	tcc	gga	cct	2670	
Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Glu	Asn	Tyr	Ser	Gly	Pro		
				505					510					515			
tat	ggg	gac	atg	cgt	ttg	gac	agt	acc	agg	gac	cac	gtt	tta	ccc	atc	2718	
Tyr	Gly	Asp	Met	Arg	Leu	Asp	Ser	Thr	Arg	Asp	His	Val	Leu	Pro	Ile		
			520					525					530				
gac	tat	tac	ttc	cca	ccc	cag	aag	acc	tgc	ctg	atc	tgt	gga	gat	gaa	2766	
Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	Glu		
		535					540					545					
gct	tct	ggc	tgt	cac	tac	gga	gct	ctc	act	tgt	ggc	agc	tgc	aag	gtc	2814	
Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val		

550	555	560	
ttc ttc aaa aga gct gcg gaa ggg aaa cag aag tat cta tgt gcc agc Phe Phe Lys Arg Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser 565 570 575 580			2862
aga aat gat tgc acc att gat aaa ttt cgg agg aaa aat tgt cca tcg Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser 585 590 595			2910
tgt cgt ctc cgg aaa tgt tat gaa gca ggg atg act ctg gga gct cgt Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg 600 605 610			2958
aag ctg aag aaa ctt gga aat ctc aaa cta cag gaa gaa gga gaa aac Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu Asn 615 620 625			3006
tcc agt gct ggt agc ccc act gag gac cca tcc cag aag atg act gta Ser Ser Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln Lys Met Thr Val 630 635 640			3054
tca cac att gaa ggc tat gaa tgt caa cct atc ttt ctt aat gtc ctg Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val Leu 645 650 655 660			3102
gaa gcc att gag cca gga gtg gtg tgt gcc gga cat gac aac aac cag Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn Gln 665 670 675			3150
cct gat tcc ttt gct gcc ttg tta tct agt ctc aac gag ctt ggc gag Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly Glu 680 685 690			3198
aga cag ctt gta cat gtg gtc aag tgg gcc aag gcc ttg cct ggc ttc Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro Gly Phe 695 700 705			3246
cgc aac ttg cat gtg gat gac cag atg gca gtc att cag tat tcc tgg Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser Trp 710 715 720			3294
atg gga ctg atg gta ttt gcc atg ggt tgg cgg tcc ttc act aat gtc Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn Val 725 730 735 740			3342
aac tct agg atg ctc tac ttt gca cct gac ctg gtt ttc aat gag tat Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu Tyr 745 750 755			3390
cgc atg cac aag tct cga atg tac agc cag tgc gtg agg atg agg cac Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg His 760 765 770			3438
ctt tct caa gag ttt gga tgg ctc cag ata acc ccc cag gaa ttc ctg Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu 775 780 785			3486
tgc atg aaa gca ctg cta ctc ttc agc att att cca gtg gat ggg ctg Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly Leu 790 795 800			3534



aaa aat caa aaa ttc ttt gat gaa ctt cga atg aac tac atc aag gaa 3582  
 Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu  
 805 810 815 820

ctt gat cgc atc att gca tgc aaa aga aaa aat ccc aca tcc tgc tca 3630  
 Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser  
 825 830 835

agg cgc ttc tac cag ctc acc aag ctc ctg gat tct gtg cag cct att 3678  
 Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro Ile  
 840 845 850

gca aga gag ctg cat caa ttc act ttt gac ctg cta atc aag tcc cat 3726  
 Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser His  
 855 860 865

atg gtg agc gtg gac ttt cct gaa atg atg gca gag atc atc tct gtg 3774  
 Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser Val  
 870 875 880

caa gtg ccc aag atc ctt tct ggg aaa gtc aag ccc atc tat ttc cac 3822  
 Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe His  
 885 890 895 900

aca cag tgaagatttg gaacctaata cccaaaccca cctgttcctt tttcagatgt 3878  
 Thr Gln

cttctgcctg ttatataact ctgcactact tctctggcat gggccttggg ggaaattcct 3938  
 ctactgatgt acagtctgtc atgaacatgt tccccaagtt ctatttcctg ggcttttcct 3998  
 tctttctttt tctttctctc tgctctttt accctcccat ggcacatttt gaatccgctg 4058  
 cgtgttggtg ctctgcctg tgttttgagt tttgttgat ttcttcaagt ctgtgatgat 4118  
 cttcttggtg cccagtgtca actgtgcttg tttatagcac tgtgctgtgt gccaaccaag 4178  
 caaatgttta ctcaccttat gccatggcaa gtttagagag ctataagtat cttgggaaga 4238  
 aacaaacaga gagagtaaaa aaaccaaaaa aaaaaaaaaa aaaccgaatt c 4289

<210> 21  
 <211> 902  
 <212> PRT  
 <213> Rattus rattus

<400> 21

Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser  
 1 5 10 15

Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu  
 20 25 30

Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ile Ala  
 35 40 45

Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg  
 50 55 60

Arg Arg Arg Gln Gln His Pro Glu Asp Gly Ser Pro Gln Ala His Ile  
 65 70 75 80

Arg Gly Thr Thr Gly Tyr Leu Ala Leu Glu Glu Glu Gln Gln Pro Ser  
 85 90 95

Gln Gln Gln Ser Ala Ser Glu Gly His Pro Glu Ser Gly Cys Leu Pro  
 100 105 110

Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro  
 115 120 125

Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser  
 130 135 140

Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile  
 145 150 155 160

Lys Asp Ile Leu Ser Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln  
 165 170 175

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln  
 180 185 190

Gln Gln Gln Glu Val Ile Ser Glu Gly Ser Ser Ser Val Arg Ala Arg  
 195 200 205

Glu Ala Thr Gly Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly  
 210 215 220

Asn Ser Thr Ile Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser  
 225 230 235 240

Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly  
 245 250 255

Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Ser Leu Leu Gly Gly Pro  
 260 265 270

Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys Lys Gly  
 275 280 285

Leu Ser Leu Asp Glu Gly Pro Gly Lys Gly Thr Glu Glu Thr Ala Glu  
 290 295 300

Tyr Ser Ser Phe Lys Gly Gly Tyr Ala Lys Gly Leu Glu Gly Glu Ser  
 305 310 315 320

Leu Gly Cys Ser Gly Ser Ser Glu Ala Gly Ser Ser Gly Thr Leu Glu  
 325 330 335

Ile Pro Ser Ser Leu Ser Leu Tyr Lys Ser Gly Ala Val Asp Glu Ala  
 340 345 350

Ala Ala Tyr Gln Asn Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ser  
 355 360 365

Gly Pro Pro His Pro Pro Pro Pro Thr His Pro His Ala Arg Ile Lys  
 370 375 380

Leu Glu Asn Pro Ser Asp Tyr Gly Ser Ala Trp Ala Ala Ala Ala Ala  
 385 390 395 400

Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Gly Ser Val Ala  
 405 410 415

Gly Pro Ser Thr Gly Ser Pro Pro Ala Thr Ala Ser Ser Ser Trp His  
 420 425 430

Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Gly Gly Gly  
 435 440 445

Gly Gly Ser Ser Ser Pro Ser Asp Ala Gly Pro Val Ala Pro Tyr Gly  
 450 455 460

Tyr Thr Arg Pro Pro Gln Gly Leu Ala Ser Gln Glu Gly Asp Phe Ser  
 465 470 475 480

Ala Ser Glu Val Trp Tyr Pro Gly Gly Val Val Asn Arg Val Pro Tyr  
 485 490 495

Pro Ser Pro Ser Cys Val Lys Ser Glu Met Gly Pro Trp Met Glu Asn  
 500 505 510

Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp His  
 515 520 525

Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile  
 530 535 540

Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly  
 545 550 555 560

Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr  
 565 570 575

Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys  
 580 585 590

Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr  
 595 600 605

Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu  
 610 615 620

Glu Gly Glu Asn Ser Ser Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln  
 625 630 635 640

Lys Met Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe  
 645 650 655

Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His  
 660 665 670

Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn  
 675 680 685

Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala  
 690 695 700

Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile  
 705 710 715 720

Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser  
 725 730 735

Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val  
 740 745 750

Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val  
 755 760 765

Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro

770

775

780

Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro  
 785 790 795 800

Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn  
 805 810 815

Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro  
 820 825 830

Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser  
 835 840 845

Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu  
 850 855 860

Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu  
 865 870 875 880

Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro  
 885 890 895

Ile Tyr Phe His Thr Gln  
 900

<210> 22  
 <211> 12  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Hypothetical oligonucleotide

<400> 22  
 gctgggttgta ag

12

<210> 23  
 <211> 4  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Hypothetical peptide

<400> 23

Ala Gly Cys Lys  
 1

E1  
 Cont

<210> 24  
<211> 32  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide probe A

<400> 24  
cttttgaaga agaccttaca gccctcacag gt 32

<210> 25  
<211> 38  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide probe B

<400> 25  
ggaccatggtt ttgcccattg actattactt tccacccc 38

<210> 26  
<211> 15  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Synthetic peptide

<400> 26

Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr  
1 5 10 15

El  
Cont